

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.76512 Seconds

(without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-21

Perfect score: 605  
Sequence: 1 MGNMATEFOOKHIIINFPILCN.....ICVKGCEQNPVHFAIGRCIP 111

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swissprot.40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585.5	36.8	111	1	RNPO_RANCA
2	451	74.5	111	1	LECS_RANJA
3	370	31.2	111	1	RNPL_RANCA
4	273.5	15.2	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANGR_MOUSE
7	136.5	22.6	145	1	ANGI_MOUSE
8	133.5	21.7	124	1	RNP_BALAC
9	129.5	21.4	124	1	RNP_PIG
10	129.5	21.4	167	1	RNBR_BOVIN
11	127.5	21.1	119	1	RNP_ICUG
12	124.5	20.6	151	1	RNBR_CAPCA
13	123.5	20.4	123	1	ANG2_BOVIN
14	123.5	20.4	141	1	RNBR_GIRCA
15	123.5	20.4	151	1	RNBR_AXIRA
16	123	20.3	146	1	ANGI_MIORA
17	120	19.8	146	1	ANGI_SAISC
18	120	19.8	147	1	ANGI_CERAE
19	120	19.8	147	1	ANGI_PONYA
20	119.5	19.8	143	1	RNBR_SHEEP
21	119	19.7	122	1	RNP_MACRU
22	118.5	19.6	123	1	ANGI_PIG
23	118.5	19.6	124	1	RNP_ANTAM
24	118	19.5	146	1	ANGI_AOTR
25	117	19.3	146	1	ANGI_SAGOE
26	116.5	19.3	128	1	RNP_MYOCO
27	116.5	19.3	149	1	RNP_MOUSE
28	115	19.0	146	1	ANGI_MACMU
29	114.5	18.9	128	1	RNBP_CAVIO
30	114	18.8	148	1	ANGI_BOVIN
31	113.5	18.8	124	1	RNP_CAMDR
32	113.5	18.8	128	1	RNP_HORSE
33	113	18.7	147	1	ANGI_HUMAN

34	113	18.7	147	1	ANGI_PANTR	O8wme8 pan troglod
35	112.5	18.6	128	1	RNP_PROGU	P04059 proechimys
36	109.5	18.1	124	1	RNP_RANPA	P00666 rangifer ta
37	109.5	18.1	146	1	ANGI_PAPHA	O8wn64 papio hamad
38	109.5	18.1	148	1	RNLA_MOUSE	O91jhl mus musculus
39	109	18.0	125	1	ANGI_RABIT	P31347 oryctolagus
40	108.5	17.9	124	1	RNP_CAPCA	P00664 capreolus c
41	108.5	17.9	124	1	RNP_GIRCA	P24717 giraffa cam
42	108.5	17.9	124	1	RNP_CITLO	P24717 citreululus
43	107.5	17.8	124	1	RNP_HUBBU	P00657 bubalus bub
44	107.5	17.8	148	1	RNP_PERLE	O9wuv5 peromyscus
45	107.5	17.8	149	1	RNP_ACOCA	O9wtts acomys cali

## ALIGNMENTS

RESULT 1  
RNPO\_RANCA STANDARD: PRT: 111 AA.  
AC P11916:  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
DE Rana catesbeiana (Bull frog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana. OX NCBI\_TaxId=8400;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Egg;  
RA MEDLINE=87299649; PubMed=3304421;  
RX Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., RA Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";  
RT Biochemistry 26:2189-2194(1987).  
RN [2]  
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
RC MEDLINE=92220613; PubMed=1373237;  
RX Liao Y.-D.;  
RA "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";  
RT Nucleic Acids Res. 20:1371-1377(1992).  
RN [3]  
RP CHARACTERIZATION.  
RC TISSUE=Egg;  
RA MEDLINE=93192604; PubMed=8448385;  
RX Nitta K., Oyama F., Sekiguchi K., Kawachi H., RA Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";  
RT Glycobiology 3:37-45(1993).  
RN [4]  
RP STRUCTURE BY NMR.  
RC MEDLINE=96437383; PubMed=9761686;  
RX Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RT "The solution structure of a cytochrome ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";  
RT J. Mol. Biol. 283:231-244(1998).  
- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.  
- SUBUNIT: MONOMER.  
- SUBCELLULAR LOCATION: Secreted.  
- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
PIR: A27121; A27121.

PDB: 1BC4: 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECFA CRC64;

Query Match 96.8%; Score 585.5; DB 1; Length 111;  
 Best Local Similarity 97.3%; Pred. No. 9.5e-57;  
 Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 2 QNMAFQOKHIINPIL-CNTILDNNIYVGGCKRVNTFTISSATTYKATCGVILNLN 60  
 DB 1 QNMAFQOKHIINPILNCNTIMDNNIYVGGCKRVNTFTISSATTYKATCGVILNMV 60  
 OY 61 LSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 111  
 DB 61 LSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 111

RESULT 2  
 LECIS\_RANJA STANDARD: PRT: 111 AA.  
 AC P18839:  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-)  
 OS Rana japonica (Japanese redbellied frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8402;  
 RN (1)  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=91035319; PubMed=2229005;  
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
 RA Takayanagi Y., Tlital K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)  
 RT eggs.";  
 RT J. Biochem. 108:139-143(1990).  
 RL -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
 CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT  
 CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0120; JX0120.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97

FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDE3634ED679 CRC64;

Query Match 74.5%; Score 451; DB 1; Length 111;  
 Best Local Similarity 77.5%; Pred. No. 3.6e-42;  
 Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

OY 2 QNMAFQOKHIINPIL-CNTILDNNIYVGGCKRVNTFTISSATTYKATCGVILNLN 59  
 DB 1 QNMAFQOKHIINPILNCNTIMDNNIYVGGCKRVNTFTISSATTYKATCGVILNMV 60  
 OY 60 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 110  
 DB 61 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 111

RESULT 3  
 RNPL\_RANJA STANDARD: PRT: 111 AA.  
 AC P14626:  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE-Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RA Okazaki T., Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)  
 RT liver.";  
 RT J. Biochem. 106:729-735(1989).  
 RL -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0085; JX0085.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 104 104  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.2%; Score 370; DB 1; Length 111;  
 Best Local Similarity 64.9%; Pred. No. 2.2e-33;  
 Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

OY 2 QNMAFQOKHIINPIL-CNTILDNNIYVGGCKRVNTFTISSATTYKATCGVILNLN 59  
 DB 1 QNMAFQOKHIINPILNCNTIMDNNIYVGGCKRVNTFTISSATTYKATCGVILNMV 60  
 OY 60 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 110  
 DB 61 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVCKENQYPVHFAGIGRC 111

RESULT 4  
 RN30\_RANPI STANDARD: PRT; 104 AA.  
 ID RN30\_RANPI  
 AC P22069;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE P-30 protein (EC 3.1.27.-) (Oncohasen).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8434;  
 RN [1]  
 RP SEQUENCE-Embryo;  
 RC TISSUE-Embryo;  
 RX MEDLINE=91093131; PubMed=1985396;  
 RA Ardelt W., Mikulski S.M., Shogen K.;  
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";  
 RL J. Biol. Chem. 266:245-251(1991).  
 RN [2]  
 RP 3D-STRUCTURE MODELING;  
 RX MEDLINE=93066156; PubMed=1438177;  
 RA Moslmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,  
 RA James M.N.G.;  
 RT "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";  
 RL Proteins 14:392-400(1992).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94160709; PubMed=8120892;  
 RA Moslmann S.C., Ardelt W., James M.N.G.;  
 RT "Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";  
 RL J. Mol. Biol. 236:1141-1153(1994).  
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.  
 CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC PDB: 1ONC; 3I-CAN-94.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom: PD000535; Rnasea; 1.  
 DR SMART: SM00092; Rnase\_Pc; 1.  
 DR PROSITE: PS00127; Rnase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; 3D-structure.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 31 31  
 FT ACT\_SITE 97 97  
 FT DISULFID 19 68  
 FT DISULFID 30 75  
 FT DISULFID 48 90  
 FT DISULFID 87 104  
 FT HELIX 3 10  
 FT STRAND 11 12  
 FT STRAND 19 22  
 FT HELIX 23 24  
 FT TURN 26 30  
 FT STRAND 33 38  
 FT STRAND 41 48  
 FT HELIX 49 50  
 FT TURN 55 58  
 FT STRAND 63 70  
 FT TURN 74 75  
 FT STRAND 77 84  
 FT STRAND 86 91  
 FT TURN 92 93  
 FT STRAND 94 101  
 SQ SEQUENCE 104 AA; 11845 MM; 22A753C2F9E56B4 CRC64;

Query Match 45.2% Score 273.5; DB 1; Length 104;  
 Best Local Similarity 48.6%; Pred. No. 5.8e-23;  
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
 Oy 2 QNATPQOKHIIHT-PIICWTILDNNIYIGGQCRVNTFLISSATVKAIGCVI-NLN 59  
 Db 1 QDMTFQKHIITTRVDVCNINSTNLF-----HKKDKNTFIYSRPEVKAIKGIASKN 56  
 Oy 60 VLSTPRLQNTCTRTSTTPPRCPYSSRTETNYICVKEKNOYPVHFGICRC 110  
 Db 57 VLTTSEFVLSDC---NVTSPRCVKYKIKKSTNKFVCTENQAPVHFGVGSQ 104  
 RESULT 5  
 ANG3\_MOUSE STANDARD: PRT; 145 AA.  
 ID ANG3\_MOUSE  
 AC P97802;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)  
 DE (EF-5).  
 GN ANG3 OR ANG1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=97184476; PubMed=9032278;  
 RA Fu X., Kamps M.P.;  
 RT "E2a-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts.";  
 RL Mol. Cell. Biol. 17:1503-1512(1997).  
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRANS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: U72672; AAC05794.1;  
 DR HSP: P10152; IAGI.  
 DR MGD: MGI:1201793; Ang1.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; Rnasea; 1.  
 DR SMART: SM00092; Rnase\_Pc; 1.  
 DR PROSITE: PS00127; Rnase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KW Protein synthesis inhibitor; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 145  
 FT MOD\_RES 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 137 137  
 FT DISULFID 50 104  
 FT DISULFID 63 115  
 FT DISULFID 81 130  
 SQ SEQUENCE 145 AA; 16696 MM; DE9D3BC92F1D682C CRC64;



[illegible]

```

Db          67  NGOTNCYGSNSTMHITDCRQFGSSKSPYCAVKAKSGEQKHIIIVACBGNPVPVPHF 120
RESULT_10
ID          RNBR_BOVIN  STANDARD:  PRT:  167 AA.
AC          P39873:
DT          01-FEB-1995 (Rel. 31, Created)
DT          01-FEB-1995 (Rel. 31, Last sequence update)
DT          16-OCT-2001 (Rel. 40, Last annotation update)
DE          Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN          BRN.
OS          Bos taurus (Mammalia).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Bovinae; Bos.
OX          NCBI_TaxID=9913;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=92093604; PubMed=1754384;
RX          Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA          Viola M., Palmieri M., Russo E., Furia A.;
RT          "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT          and its expression in different regions of the brain.";
RL          Nucleic Acids Res. 19:6469-6474(1991).
RN          [2]
RP          SEQUENCE OF 27-167; AND CARBOHYDRATE-LINKAGE SITES.
RP          TISSUE=Brain;
RC          MEDLINE=89214015; PubMed=3243767;
RX          Watanabe H., Katoh H., Ishii M., Komoda Y., Sada A., Takizawa Y.,
RA          Ohki K., Irie M.;
RT          "Primary structure of a ribonuclease from bovine brain.";
RL          J. Biochem. 104:939-945(1988).
RN          [3]
RP          SEQUENCE OF 27-167 FROM N.A.
RX          MEDLINE=96139017; PubMed=8587129;
RA          Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,
RA          Vento M.T., Furia A.;
RT          "Molecular evolution of genes encoding ribonucleases in ruminant
RT          species.";
RL          J. Mol. Evol. 41:850-858(1995).
CC          -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
CC          modified and this statement is not removed. Usage by and for commercial
CC          entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC          or send an email to license@isb-sib.ch).
CC          -----
DR          EMBL; X59767; CAA42439.1; -.
DR          EMBL; S81744; AAB36138.1; -.
DR          PIR; S20066; S20066.
DR          PIR; JX0056; JX0056.
DR          HSSP; P00656; 2RNS.
DR          GlycoSuiteDB; P39873; -.
DR          InterPro; IPR001427; RNaseA.
DR          Pfam; PF00074; rnaaseA.1.
DR          PRINTS; PR00794; RIBONUCLEASE.
DR          PRODOM; PD000535; RNaseA; 1.
DR          SMART; SM00092; RNaseA_Pc; 1.
DR          PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW          Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT          CHAIN 1 26
FT          SIGNAL 1 26
FT          ACT_SITE 27 167 RIBONUCLEASE, BRAIN.
FT          ACT_SITE 38 38 BY SIMILARITY.
FT          ACT_SITE 67 67 BY SIMILARITY.
FT          ACT_SITE 145 145 BY SIMILARITY.
FT          DISULFID 52 110 BY SIMILARITY.
FT          DISULFID 66 121 BY SIMILARITY.
FT          DISULFID 84 136 BY SIMILARITY.
FT          DISULFID 91 98 BY SIMILARITY.

```

[illegible]

Db 1 QDMSFQNKHIDPETSASNPAYCDLMQOR-NLNPCKCTNTFVHASPEIQVCGS 59  
 OY 53 --TGVINLNTSTRFOLNTCTRTST-PRCPYSSRTETNYCVGCENQYPVHF 104  
 Db 60 GGHYEDNLIDYSDLDLDCRKNVGTAPSSCKYNGTPTGKRIRIACENNQPVHF 114

## RESULT 12

RNRB\_CARCA

ID RNRB\_CARCA STANDARD: PRT: 151 AA.

AC P79351;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ribonuclease, brain (EC 3.1.27.-) (BRB).

OS Capreolus capreolus (Roe deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;

OC Cervidae; Odocolleinae; Capreolus;

OX NCBI\_TaxID=9853;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98278842; PubMed=9611265;

RA Beukelman H.J., van der Munnik N., Kleiendam R.G., Furia A.,

RA Beukelman J.J.;

RT "Secretory ribonuclease genes and pseudogenes in true ruminants."

RL Gene 212:259-268(1998).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC CC

DR EMBL: Y11673; CAA72371.1;

DR HSSP: P00656; ISRN.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

DR KMHYDrolase; Nuclease; Endonuclease; Glycoprotein.

FT ACT\_SITE 41 41

FT DISULFID 26 84

FT DISULFID 40 95

FT DISULFID 58 110

FT DISULFID 65 72

FT CARBOHYD 125 62

FT CARBOHYD 133 129

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

FT CARBOHYD 133 133

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiotensin-2 (EC 3.1.27.-) ANG2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovine; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=97409980; PubMed=9266695;

RA Strydom D.J., Bond M.D., Vallee B.L.;

RT "An angiotensin protein from bovine serum and milk -- purification and

RT primary structure of angiotensin-2."

RL Eur. J. Biochem. 247:535-544(1997).

CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND

CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC

CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND

CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY

CC HYDROLYZING CELLULAR TRNAS.

CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR HSSP: P10152; IAGI.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

DR KMHYDrolase; Nuclease; Endonuclease; Angiogenesis;

DR KW Protein synthesis inhibitor; Glycoprotein.

FT ACT\_SITE 12 12

FT ACT\_SITE 39 39

FT ACT\_SITE 113 113

FT DISULFID 25 80

FT DISULFID 38 91

FT DISULFID 56 106

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

Query Match 20.4%; Score 123.5; DB 1; Length 123;  
 Best Local Similarity 29.6%; Pred. No. 1.3e-06;  
 Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;

## RESULT 14

RNRB\_GIRCA

ID RNRB\_GIRCA STANDARD: PRT: 141 AA.

AC Q29542; Q29533;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ribonuclease, brain (EC 3.1.27.-) (BRB).

OS BRN.

OC Giraffa camelopardalis (Giraffe).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffidae;

OC Giraffidae; Giraffe.

OX NCBI\_TaxID=9894;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97409980; PubMed=9266695;

RA Strydom D.J., Bond M.D., Vallee B.L.;

RT "An angiotensin protein from bovine serum and milk -- purification and

RT primary structure of angiotensin-2."

RL Eur. J. Biochem. 247:535-544(1997).

CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND

CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC

CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND

CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY

CC HYDROLYZING CELLULAR TRNAS.

CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR HSSP: P10152; IAGI.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

DR KMHYDrolase; Nuclease; Endonuclease; Angiogenesis;

DR KW Protein synthesis inhibitor; Glycoprotein.

FT ACT\_SITE 12 12

FT ACT\_SITE 39 39

FT ACT\_SITE 113 113

FT DISULFID 25 80

FT DISULFID 38 91

FT DISULFID 56 106

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

FT CARBOHYD 33 33

```

RX MEDLINE:96139017; PubMed=8587129;
RA Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
species.";
J. Mol. Evol. 41:850-858(1995).
RL
RM
RN
RP SEQUENCE OF 31-114 FROM N.A.
RX MEDLINE:93367815; PubMed=8360916;
RA Breukelman H.J., Belmonte J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
the genomic DNA of mammalian species.";
J. Mol. Evol. 37:29-35(1993).
CC
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: S81743; AAB36137.1; -
DR EMBL: S65126; AAB27931.1; -
DR HSSP: P00656; 2RNS.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR PRINTS: PRO0794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACET. SITE 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EEF9079591P CRC64;

Query Match 20.4%; Score 123.5; DB 1; Length 141;
Best Local Similarity 29.8%; Pred. No. 1.5e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

QY 5 ATFOOKHL-----INPIICITLIDNNIYIVGGCKKRVNFTIISATTVAICTGVNL 58
Db 6 AKFRROHMDSSSSSSNSNCGNMKKR-RMTHGRCKRVNFVHESLADVAKVS---QK 61

QY 59 NVL-----STRQLNTCTRTSTTPRP-CYISRTETNICYKE-NQY-PVHFA 105
Db 62 NITKKGQPCNYGSNSTWNITIDCRETGSSKYPNCAYKTSOKQITVACEGNPYVPVPHD 121
QY 106 G 106
Dy 122 G 122

RESULT 15
RNBR_AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Axis.

```

```

RN NCBI_TaxID=57737;
RP [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=98278842; Pubmed=9611269;
RA Breukelman H.J., van der Munnik N., Kleinedam R.G., Furia A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-260(1998).
CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on ways
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; Y11670; CAAT72368.1; -.
DR HSSP; P00656; ISRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACY_SITE 41
FT DISULFID 26
FT DISULFID 40
FT DISULFID 84
FT DISULFID 95
FT DISULFID 58
FT DISULFID 110
FT DISULFID 65
FT CARBOHYD 72
FT CARBOHYD 62
FT CARBOHYD 129
FT CARBOHYD 133
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FFC5B233 CRC64;
Query Match 20.4%; Score 123.5; DB 1; Length 151;
Best Local Similarity 29.8%; Pred. No. 1.6e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;
OY 5 ATFOQKH-----INPIICNTILDNNIIVGQCCKRVNFTIISATTVAICTGVNL 58
Db 6 AKFRROHMDAGSSSGNSNYCNOMKKRR-RMTWGRCKRVPNFVHESLDSVKAACS---QK 61
OY 59 NVL-----STPRFLNCTCRTSITPR-CPSRSRETNLYCKE-NQY-PVFA 105
Db 62 NITTKNOPNCYGQSNSTMNITDCRETGGSKTPNCAYIKTSOKAKITIYACENPTYPVAFD 121
OY QY 106 G 106
Db Db 122 G 122

```